

Specific Volumes of Proteins and the Relationship to their Amino Acid Contents

T. L. McMeekin and Kathleen Marshall

*Eastern Regional Research Laboratory,¹
Philadelphia, Pennsylvania*

The specific volume of a protein is essential for calculating its molecular weight in solution and for relating the composition of a protein crystal to its density. Values for specific volumes are obtained experimentally from density measurements. Cohn and Edsall (1) have, however, described a method for calculating the specific volume of a protein from its amino acid composition, the volume of the protein molecule being considered to be the sum of the volumes of its component groups or atoms. At the time of publication of this method for calculating specific volumes of proteins from their amino acid compositions, the data on the amino acid composition of proteins were incomplete and unreliable. During the past ten years, new methods, such as the use of isotopes, bacteria, and chromatography, in the determination of amino acids have led to reliable and fairly complete amino acid analysis on a large number of proteins. It became of importance and interest, therefore, to test the method for calculating specific volumes of proteins using recent quantitative amino acid composition data. Values obtained for the specific volume of a number of proteins calculated from their amino acid composition are compared in Table 1 with the observed values obtained by density measurements. It may be noted that in most cases the values calculated from the amino acid composition are in excellent agreement with the observed values. The differences between the observed and calculated values for the last three proteins in the table are greater than might be expected in view of the other results and suggest that the amino acid composition and specific volume for these three proteins be redetermined.

The method for calculating a specific volume from the amino acid composition neglects electrostriction that is due to charged groups in the protein molecule; consequently, it might be expected that the calculated value for the specific volume would be higher than that observed. Cohn and Edsall (1) calculated that the value of the specific volume of egg albumin in solution would be reduced by 2.4% because of electrostriction. The value for electrostriction in other pro-

¹ One of the laboratories of the Bureau of Agricultural and Industrial Chemistry, Agricultural Research Administration, U. S. Department of Agriculture.

TABLE 1
SPECIFIC VOLUME OF PROTEINS

Protein	Sp vol observed* (cc/g)	Sp vol calcd from amino acid com- position† (cc/g)
Silk fibroin		
(suspended in H ₂ O)	0.701 (2)	0.689 (3)
Ribonuclease	.709 (4)	.703 (3)
Wool (suspended in H ₂ O)	.716 (5)	.712 (3)
Lysozyme	.722 (6)	.717 (7)
Fibrinogen (human)	.725 (8)	.723 (3)
α-Casein	.728 (9)	.725 (9)
Chymotrypsinogen	.73 (10)	.734 (3)
Casein (unfractionated)	.731 (9)	.731 (9)
Serum albumin (bovine)	.734 (11)	.734 (12)
Insulin (Zn)	.735 (13)	.724 (3)‡
D-glyceraldehyde phosphate dehydrogenase	.737 (11)	.743 (11)
Aldolase	.740 (11)	.743 (11)
β-Casein	.741 (9)	.743 (9)
Ovalbumin	.745 (14)	.738 (3)
Hemoglobin (horse)	.749 (15)	.741 (3)§
β-Lactoglobulin	.751 (16)	.746 (17)
Botulinus toxin	.75 (18)	.736 (18)
Gelatin	.682 (19)	.707 (3)
Edestin	0.744 (20)	0.719 (3)

* These values were determined at 20° C, or close thereto.
† With the exception of references (9), (11), and (18), the specific volume values have been calculated from the amino acid compositions given in the cited reference. A value of 0.63 cc was used for the volume of the cystine residue instead of 0.61 cc, as given in Cohn and Edsall (1).

‡ The specific volume of zinc is not included.

§ The specific volume of hemin is not included.

teins would vary slightly owing to the number of charged groups in the molecule. Linderström-Lang (21) observed that the initial enzymic hydrolysis of a protein involves a large change in volume per mole of peptide bond split (-50 cc). The preponderance of the peptide bonds in the protein, however, was found to give the normal contraction in volume when split (-20 cc); accordingly, the total effect of this volume factor on the specific volume of the protein would not be expected to be large. The excellent agreement between the calculated and observed values for the specific volumes of proteins may be due in part, therefore, to a compensation of variables.

The fact that the values for the volumes of proteins obtained by these two methods agree for such a wide variety of proteins is considered to be good evidence that the volume of a protein molecule in solution is essentially equal to the sum of the volumes of its component groups and that the method of Cohn and Edsall for calculating specific volumes is reliable.

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